

Genome version 4.1
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OM protein - protein search, using SW model

Run on: January 17, 2002, 08:00:09 : User Name: 23-78 Seconds

With 10000 alignments
5,555 Million cell updates/sec

Title: US-09-674-436-1

Protein Score: 1 BLK 5

Scoring Method: PROSPP62

Gaped 10.0, Gapex 0.5

Sequences: 522453 seqs, 7407390 residues

Total number of hits satisfying chosen parameters: 522453

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A_Geneseq.1101*

```

1: 751587/43674436-1:protein:AA1587.101*
2: 751587/43674436-1:protein:AA1587.101*
3: 751587/43674436-1:protein:AA1587.101*
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5: 751587/43674436-1:protein:AA1587.101*
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22: 751587/43674436-1:protein:AA1587.101*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length (B)	ID	Description
1	25	100.0	5	21	AAV75478
2	25	100.0	5	22	AAV75478
3	25	100.0	124	21	AAV12727
4	25	100.0	127	21	AAV12726
5	25	100.0	142	21	AAV12725
6	25	100.0	158	16	AAV75435
7	25	100.0	179	16	AAV75434
8	25	100.0	180	17	AAV75433
9	25	100.0	181	15	AAV75432
10	25	100.0	186	21	AAV75431
11	25	100.0	186	21	AAV75430

12	25	100.0	187	21	AAV75429
13	25	100.0	187	21	AAV75428
14	25	100.0	194	16	AAV75427
15	25	100.0	194	16	AAV75426
16	25	100.0	194	16	AAV75425
17	25	100.0	194	16	AAV75424
18	25	100.0	202	11	AAV75423
19	25	100.0	202	11	AAV75422
20	25	100.0	202	11	AAV75421
21	25	100.0	202	11	AAV75420
22	25	100.0	202	11	AAV75419
23	25	100.0	202	11	AAV75418
24	25	100.0	202	11	AAV75417
25	25	100.0	202	11	AAV75416
26	25	100.0	202	11	AAV75415
27	25	100.0	202	11	AAV75414
28	25	100.0	202	11	AAV75413
29	25	100.0	202	11	AAV75412
30	25	100.0	202	11	AAV75411
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35	25	100.0	202	11	AAV75406
36	25	100.0	202	11	AAV75405
37	25	100.0	202	11	AAV75404
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43	25	100.0	202	11	AAV75398
44	25	100.0	202	11	AAV75397
45	25	100.0	202	11	AAV75396

[illegible]

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Query Match	100.00%	Score 251.26	100.00%	100.00%			
Fast Local Similarity	100.00%	Prod. No. 100	20	10.00%			
Matches	51	Conservation	2	Mismatches	10	10.00%	100%
QY	1	DIRS 5					
LE	96	difs 100					
PERSIML	5						
AA012725							
XX	AA012725 standard; Protein: 146 AA.						
XX	AA012725:						
XX	17-OCT-2000 (first entry)						
XX	Arabidopsis thaliana Proteins: Truncated Shc - N-terminus						
XX	Protein Identification: Signal Transduction Pathways and Kinase Pathways						
XX	hybridization assay: growth for multipoint growth of cells in 96-well plates						
XX	termination sequence						
XX	Arabidopsis thaliana						
XX	EP1033405-A2						
XX	66-SEP-2000:						
XX	25-FEB-2000: 2000Feb-20144						
XX	25-FEB-1999: 991S-0149-21						
XX	05-MAR-1999: 991S-0141-80						
XX	09-MAR-1999: 991S-0140-46						
XX	23-MAR-1999: 991S-0125-98						
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XX	08-APR-1999: 991S-0128-11						
XX	16-APR-1999: 991S-0129-45						
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XX	03-JUN-1999: 991S-0137-22						
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XX	10-JUN-1999: 991S-0138-94						

[illegible]

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3	0	0	1

[illegible][illegible][illegible]

Author	Year	Country	Sample Size	Study Design	Findings
Smith, M. J.	1995	USA	100	Experimental	High level of similarity between groups
Johnson, L. A.	1998	USA	150	Experimental	High level of similarity between groups
Miller, R. D.	2001	USA	200	Experimental	High level of similarity between groups
Wilson, K. E.	2003	USA	250	Experimental	High level of similarity between groups
Anderson, J. B.	2005	USA	300	Experimental	High level of similarity between groups
Thompson, S. C.	2007	USA	350	Experimental	High level of similarity between groups
White, H. G.	2009	USA	400	Experimental	High level of similarity between groups
Black, D. L.	2011	USA	450	Experimental	High level of similarity between groups
Green, E. F.	2013	USA	500	Experimental	High level of similarity between groups
Gray, I. H.	2015	USA	550	Experimental	High level of similarity between groups
King, J. K.	2017	USA	600	Experimental	High level of similarity between groups
Lee, M. N.	2019	USA	650	Experimental	High level of similarity between groups
Wong, P. Q.	2021	USA	700	Experimental	High level of similarity between groups
Yip, R. S.	2023	USA	750	Experimental	High level of similarity between groups
Zhang, T. U.	2025	USA	800	Experimental	High level of similarity between groups

[illegible]

Ref.	Model	Year	Country	Sample Size	Model
[1]	AAE(1,1,0,0)	1971-1997	USA	27	AA
[2]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[3]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[4]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[5]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[6]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[7]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[8]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[9]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[10]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[11]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[12]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[13]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[14]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[15]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[16]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[17]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[18]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[19]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[20]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[21]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[22]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[23]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[24]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[25]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[26]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[27]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[28]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[29]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[30]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[31]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[32]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[33]	AAE(1,0,0,0)	1971-1997	USA	27	AA
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[45]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[46]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[47]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[48]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[49]	AAE(1,0,0,0)	1971-1997	USA	27	AA
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[52]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[53]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[54]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[55]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[56]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[57]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[58]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[59]	AAE(1,0,0,0)	1971-1997	USA	27	AA
[60]	AAE(1,0,0,0)				

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible][illegible]

the 1990s, the number of people in the world who are undernourished has declined from 1.1 billion to 800 million. The number of people who are malnourished has declined from 1.5 billion to 1.1 billion. The number of people who are obese has increased from 100 million to 300 million. The number of people who are overweight has increased from 100 million to 300 million. The number of people who are obese and overweight has increased from 100 million to 300 million. The number of people who are obese and overweight has increased from 100 million to 300 million.

[illegible][illegible][illegible][illegible][illegible][illegible]

As a result, the authors conclude that the use of the *in vitro* model is not sufficient to predict the *in vivo* behavior of the system. The authors suggest that the use of a *in vivo* model is necessary to determine the effect of the system on the host.

[illegible]

XX Sequence 194 AAs

Query Match: 100.0%; Score 25; Id 1; Length 194;
Best Local Similarity: 100.0%; Pred. No. 1; 100.0%;
Matches 5; Mismatched 0; Mismatches 0; Gaps 0;

Q7 1 D11K6 5
1111
DB 121 diff 125

RESULT 15

AA75345
ID AA75345 standard: Protein: 194 AAs.

AC AA75345;

DI 13-DEC-1995 (first entry)

DE Hybrid human cytokine IL1E.

KW Hybrid cytokine; tumour proliferation; cancer therapy.

OS Synthetic.

PH Key Location/Qualifiers

FI Misc-difference 132

PN W09513444-A.

PD 18-MAY-1995.

PF 07-NOV-1994; 94WO-051287A.

PR 08-NOV-1994; 94OS-0149101.

PA (HUT-) HUTCHINSON CANCER RES CENTER ERHD.

PI Leung JW, Rosen JM, Tedaro GJ;

DR WPI: 1995-19411/25.

DR N-PSDB: AA75345.

PI New hybrid cytokines with alpha helical segments from different

PT sources - also DNA encoding them, vectors and T-activated cells,

PS Claim 11; Page 33-34; 52pp; English.

CC The cytokine encoding genes for leukemia inhibitory factor (LIF),

CC granulocyte colony stimulating factor (G-CSF), interleukin 6 (IL-6),

CC interleukin-11 (IL-11), ciliary neurotrophic factor (CNTF) and

CC oncostatin M (OS) have been cloned and reported in the literature.

CC LIF, G-CSF, IL-6 and CNTF each comprise four alpha helical sequences. In

CC each cytokine, the four alpha helical sequences are linked by non-

CC alpha-helical "linking" sequences of about 5-10 AAs. The invention

CC provides a group of the above hybrid cytokines having a size ranging

CC from about 19 to about 30 kDa. Each hybrid cytokine comprises three or

CC four alpha-helical sequences and linking sequences, ranging from about

CC 5-10 AAs in length. In the nomenclature of the hybrid cytokines,

CC upper case letters designate alpha-helical segments, lower case

CC letters (whether Arabic numerals, alphabets or symbols) indicate

CC a specific linking sequence. The first three alpha-helical

CC sequences of IL1E were derived from ILF, and the fourth

CC alpha-sequence was derived from IL-11.

XX Sequence 194 AAs

Best Local Similarity: 100.0%; Score 25; Id 1; Length 194;
Matches 5; Mismatched 0; Mismatches 0; Gaps 0;

Q7 1 D11K6 5
1111
DB 121 diff 125

Search completed: January 22, 2002 07:43:15
Job time: 009 sec

Query Match:

100.0%; Score 25; Id 1; Length 194;

NAME/KEY: 11-11-11
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Query Match	100.0%	Score 25	100.0%	Length 249
Best Local Similarity	100.0%	Prod. No. 1		
Matches	0	Mismatches	0	Gaps 0

Query Match	100.0%	Score 25	100.0%	Length 249
Best Local Similarity	100.0%	Prod. No. 1		
Matches	0	Mismatches	0	Gaps 0

Query Match	100.0%	Score 25	100.0%	Length 249
Best Local Similarity	100.0%	Prod. No. 1		
Matches	0	Mismatches	0	Gaps 0

QY	1111105
	11111
DB	15511110155

QY	1111105
	11111
DB	15511110155

RECEIVED 1977

E83469
hypothetical protein PA1406 [Imported] - Pseudomonas aeruginosa (Strain PAO)
of Genes; pseudomonas_aeruginosa

C: Species: *Pseudomonas aeruginosa*

C:\Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
C:\Account: 194460 #seq_ext_date 31-Dec-2000

C:\ACCESS\LOU: F84469

RISTOVIC, G. K., PHAM, X. G., DEJIC, A. L., MICHAELOPOULOS, D., KATZ, P. H., KONG, M., and KIM, J. H. 2003. A new species of the genus *Phrynosoma* from the Yucatán Peninsula, Mexico. *Journal of Herpetology* 37: 109–119.

LODY, S.: OLSON, M.V.
NATURE 406 4454-4464 2003

Nature 406, 959-964, 2000

A: Reference number: AB22950; M1111-20447347
A1: title: Complete genome sequence of *Pseudomonas* cf. *cinosa* PA01, an opportunistic patho

A: Accession: F83464

A:Accession: E83454
A:Status: preliminary

A: Molecule type: DNA
A: Status: preliminary

A: Molecule type: DNA
A: Residues: 1-2500

A; Residues: 1-252 (SI)

A/Cross-references: 03.AB00470, 03.AB00491, 41111-14740, 4111N.AB00475...; 41111: 2N-1
A/Cross-references: 03.AB00470, 03.AB00491, 41111-14740, 4111N.AB00475...; 41111: 2N-1
A/Cross-references: 03.AB00470, 03.AB00491, 41111-14740, 4111N.AB00475...; 41111: 2N-1

A: Experimental source: strain PA01
C: Phages:

C: Genetics:
A: General: Biology

A: 01-11-2016: 12:41:43

Query Match	100.0%	Score: 257	JB	Length: 2527
Post Local Similarity	100.0%	Prod. NO.	100.0%	
Matches	5	Conservative	0	Mismatches
				Indels
				Gaps

Query Match	100.0%	Score: 257	JB	Length: 2527
Post Local Similarity	100.0%	Prod. NO.	100.0%	
Matches	5	Conservative	0	Mismatches
				Indels
				Gaps

Query Match	100.0%	Score: 257	JB	Length: 2527
Post Local Similarity	100.0%	Prod. NO.	100.0%	
Matches	5	Conservative	0	Mismatches
				Indels
				Gaps

cy 1 M.R. 5
11111
db. 188 M.R. 192

cy 1 M.R. 5
11111
db. 188 M.R. 192

Search completed: January 17, 2002, 08:11:16
Job time: 122 sec

Job time: 122 sec.

GenCode version 4.1
Copyright (c) 1995 - 2000 Cambridge University

an protein - protein search, using sw model

Run on: January 17, 2002, 08:09:44 ; 100% ; 10.16 seconds

$$S_{\text{eff}} = \int d^4x \sqrt{-g} \left[\frac{1}{2} R - \frac{1}{2} (\partial_\mu \phi)^2 - V(\phi) \right]$$

Title: US-09-674 436-1

Sequence: 1.D1.R0

Scoring table: MLossUM62
 Cmapop 10.33 - Cmapext 0.5

Searched: 100059 soqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

	Minimum	I/O Seq	Length:
Maximum I/O Seq	108	108	108

Maximum DB Seq Length: 20,000,000

Post-processing: Minimum Match 08
Maximum Match 100%

Maximum Males, 1004

Listed first, 45 summaries

Database : SwissProt_49:★

pred. No. is the number of results predicted to have a score greater than or equal to the score of i result being predicted and is derived by analysis of the total results distribution.

SUMMARY

Result	No.	Score	Country	Match	Length	DB	110
	1	25	199.0	150	1	CNRD_MOUSE	
	2	25	199.0	193	1	YK18_YEAST	
	3	25	199.0	197	1	YS92_METJA	
	4	25	198.0	202	1	LIF_HUMAN	
	5	25	199.0	202	1	LIF_MOUSE	
	6	25	100.0	235	1	HT10_PROEC	
	7	25	199.0	310	1	CHIL2_PTYAB	
	8	25	100.0	312	1	N1K1_AZSCA	
	9	25	100.0	340	1	Y117_HERAD	
	10	25	100.0	340	1	Y117_HERAD	
	11	25	100.0	427	1	ABGA_STRPN	
	12	25	100.0	430	1	AR_6_PACLA	
	13	25	100.0	446	1	BC14_HUMAN	
	14	25	100.0	658	1	BM12_HUMAN	
	15	25	100.0	1050	1	LKTA_ACIAC	
	16	25	100.0	1305	1	GAK_FAT	
	17	25	100.0	1574	1	MY52_YEAST	
	18	25	100.0	1765	1	CYAO_PPCPR	
	19	25	100.0	1766	1	CYAO_PPCPR	
	20	25	100.0	2116	1	R0H1_STYV	
	21	24	96.0	202	1	L11_HOVIN	
	22	24	96.0	310	1	Y125_STK03	
	23	24	96.0	413	1	V11P_RHSEN	
	24	24	96.0	429	1	N141_AZSCA	
	25	24	66.0	352	1	1P0P_W911P	
	26	24	96.0	365	1	BE12_DSCOL	
	27	24	96.0	381	1	P1X1_HUMAN	
	28	24	96.0	381	1	P1X1_MOUSE	
	29	24	96.0	402	1	YXAH_BACSU	
	30	24	96.0	434	1	TH02_AQJAE	
	31	24	96.0	437	1	Y0Y1_BAUSG	
	32	24	96.0	452	1	H157_PUWPK	
	33	24	96.0	453	1	H158_KAT	
Legend							
656937	mus_musculi						
616149	gallus_gallus						
Q58287	can_familiaris						
F15018	homo_sapiens						
Q62728	mus_musculi						
Q57065	photinus_luminosa						
Q70766	pyricularia_oryzae						
P13217	arabidopsis_thaliana						
Q72010	homo_sapiens						
Q72010	homo_sapiens						
F13395	staphylococcus_aureus						
Q20749	homo_sapiens						
Q72255	homo_sapiens						
P16462	actinobolus_saccharum						
P17474	rattus_norvegicus						
P15434	saccharomyces_cerevisiae						
Q57506	borostoma_melanocephala						
P15418	borostoma_melanocephala						
P31342	sonchus_oleraceus						
Q27936	bovis_taurus						
Q52435	staphylococcus_aureus						
Q53141	thelocadmus						
Q57765	gryllus_bimaculatus						
Q57698	mus_musculi						
P27212	oscarota_ferula						
P26012	homo_sapiens						
Q48729	mus_musculi						
P42107	bacillus_subtilis						
Q67409	agrobacterium_tumefaciens						
P21541	halobacterium_salinarum						
P28524	phycomyces_thermophilus						
P17105	rattus_norvegicus						

34	24	96.0	4.7	MM1	bc_vin	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
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ALLIANCE

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RESIDUE 1
NMID: MOUSE
ID: CNR_MOUSE STANFORD PRJ: 140 AA
OS: 05/05/92
DT: 15-JUN-1999 (Revised)
DI: 15-JUN-1999 (Revised)
DI: 20-AUG-2001 (Revised)
DE: RETINAL ROD PHOTORECEPTOR CATALYTIC SUBUNIT (RHO)
DE: BETA SUBUNIT (PDB: 1A17) (CNR: 00000117)
CN: PDBID.
Mus musculus (Mouse).
Eukaryotic. Molecular Weight: 37,400.
Recombinant. Produced by recombinant technology.
OS: NCBI_TaxID: 10090;
ID: 11
SEQUENCE FROM N.A.
KA: MEDLINE: 9623343; PubMed: 957051;
KA: Li, N.; Foltz, S.R.; Schmitt, M.; Fan, H.; Fong, A.; Gao, W.;
KT: "Characterization of human and mouse rod opsin (photodiode) gene and its
KT: subunit (PDBid) and chromosomal localization of the human gene."
KL: Genomics 49:76-82(1998).
KN: 12)
SEQUENCE FROM N.A.
KA: MEDLINE: 9645414; PubMed: 9706443;
KA: Lottor, B.; Maltzman, E.; Johnson, F.; Brown, A.; Farnham, J.;
KA: D'Amico, M.; Bock, J.; Finkelstein, A.; Poll, J.;
KT: "Cloning and sequence of the rod opsin (PDBid) gene and its
KT: subunit gene (PDBid) in man and mouse."
KL: Eur. J. Hum. Genet. 7:283-294(1999).
KN: 13)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 14)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 15)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 16)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 17)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
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KT: GENOMICS 49:76-82(1998).
KT: 18)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 19)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 20)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
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KT: GENOMICS 49:76-82(1998).
KT: 21)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 22)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 23)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
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KT: GENOMICS 49:76-82(1998).
KT: 24)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 25)
KA: MEDLINE: 9645414; PubMed: 9706443;
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KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
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KT: GENOMICS 49:76-82(1998).
KT: 26)
KA: MEDLINE: 9645414; PubMed: 9706443;
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KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
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KT: GENOMICS 49:76-82(1998).
KT: 27)
KA: MEDLINE: 9645414; PubMed: 9706443;
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KT: GENOMICS 49:76-82(1998).
KT: 28)
KA: MEDLINE: 9645414; PubMed: 9706443;
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KT: GENOMICS 49:76-82(1998).
KT: 29)
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KT: GENOMICS 49:76-82(1998).
KT: 30)
KA: MEDLINE: 9645414; PubMed: 9706443;
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KT: GENOMICS 49:76-82(1998).
KT: 31)
KA: MEDLINE: 9645414; PubMed: 9706443;
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KT: GENOMICS 49:76-82(1998).
KT: 32)
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KT: 33)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 34)
KA: MEDLINE: 9645414; PubMed: 9706443;
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KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 35)
KA: MEDLINE: 9645414; PubMed: 9706443;
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KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 36)
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KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 37)
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KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 38)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG, A.; GAO, W.;
KT: "CHARACTERIZATION OF HUMAN AND MOUSE ROD OPSON (PHOTODIODE) GENE AND ITS
KN: CHROMOSOMAL LOCALIZATION OF THE HUMAN GENE."
KT: GENOMICS 49:76-82(1998).
KT: 39)
KA: MEDLINE: 9645414; PubMed: 9706443;
KT: "CAVALLI, A.; FOLTZ, S.R.; SCHMITT, M.; FAN, H.; FONG
```

140 10 JUL80 14

141

142 FROM: YEAH

143 TO: YEAH

144 FROM: YEAH

145 TO: YEAH

146 FROM: YEAH

147 TO: YEAH

148 FROM: YEAH

149 TO: YEAH

150 FROM: YEAH

151 TO: YEAH

152 FROM: YEAH

153 TO: YEAH

154 FROM: YEAH

155 TO: YEAH

156 FROM: YEAH

157 TO: YEAH

158 FROM: YEAH

159 TO: YEAH

160 FROM: YEAH

161 TO: YEAH

162 FROM: YEAH

163 TO: YEAH

164 FROM: YEAH

165 TO: YEAH

166 FROM: YEAH

167 TO: YEAH

168 FROM: YEAH

169 TO: YEAH

170 FROM: YEAH

171 TO: YEAH

172 FROM: YEAH

173 TO: YEAH

174 FROM: YEAH

175 TO: YEAH

176 FROM: YEAH

177 TO: YEAH

178 FROM: YEAH

179 TO: YEAH

180 FROM: YEAH

181 TO: YEAH

182 FROM: YEAH

183 TO: YEAH

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185 TO: YEAH

186 FROM: YEAH

187 TO: YEAH

188 FROM: YEAH

189 TO: YEAH

190 FROM: YEAH

191 TO: YEAH

192 FROM: YEAH

193 TO: YEAH

194 FROM: YEAH

195 TO: YEAH

196 FROM: YEAH

197 TO: YEAH

198 FROM: YEAH

199 TO: YEAH

200 FROM: YEAH

201 TO: YEAH

202 FROM: YEAH

203 TO: YEAH

204 FROM: YEAH

205 TO: YEAH

RA Bentley D., Scheel P.: The EMBL/GenBank/DDBJ databases.
 RI Submitted (Jan 1993) 1. The EMBL/GenBank/DDBJ databases.
 RN [5]
 RX SEQUENCE OF 8-202 FROM N.A.
 RA MEDLINE:88190120; PubMed:3128791;
 RA Gough N.M., Gearing D.P., King J.A., Williams J., Wilson G.
 RA Nicola N.A., Metcalf D.J.
 RI "Molecular cloning and expression of the human homologue of the
 RI murine gene encoding myeloid leukemia inhibitory factor."
 RI Proc. Natl. Acad. Sci. U.S.A. 85:12623-12627(1988).
 RN [6]
 RX SEQUENCE OF 23-49.
 RA MEDLINE:89256299; PubMed:3739799.
 RA Mori M., Yamaguchi K., Abe K.:
 RI "Purification of a lipoprotein lipase inhibitor protein produced by
 RI a melanoma cell line associated with cancer cachexia."
 RI Biochem. Biophys. Res. Commun. 160:1085-1092(1989).
 RN [7]
 RX SEQUENCE BY NAME OF HUMAN HOUSE CHIMERA.
 RA MEDLINE:98256299; PubMed:9597315.
 RA Birds M.G., Maurer T., Zhang J.G., Nicola N.A., Norton K.S.:
 RI "Solution structure of leukemia inhibitory factor."
 RI J. Biol. Chem. 273:13738-13745(1998).
 CC -1- FUNCTION: LIF HAS THE CAPACITY TO INHIBIT HEMATOPOIETIC DIFFERENTIATION
 CC IN LEUKEMIC CELLS. ITS ACTIVITIES INCLUDE THE INDUCTION OF
 CC HEMATOPOIETIC DIFFERENTIATION IN NORMAL AND MYELOID LEUKEMIA
 CC CELLS, THE INDUCTION OF NEURONAL CELL DIFFERENTIATION, AND THE
 CC STIMULATION OF ACUTE-PHASE PROTEIN SYNTHESIS IN HEPATOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE LIF / OSM FAM IN
 CC
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 DR EMBL: X14647; CAA33147.1;
 DR EMBL: J01261; AAA58517.1;
 DR EMBL: M27053; AAA53188.1;
 DR EMBL: M27053; AAA53188.1; J01NPP.
 DR EMBL: A2004264; AAC05174.1;
 DR EMBL: M61420; AAA51699.1;
 DR PIR: R34292; B36293.
 DR PIR: S06460; S06460.
 DR PIR: JATM; 20-APP-96.
 DR MIM: 159540;
 DR InterPro: IPR001581; LIF_OSM.
 DR Pfam: PF01291; LIF_OSM.1.
 DR SMART: SM00080; LIF_OSM.1.
 DR PROSITE: PS00590; LIF_OSM.1.
 KW Tyrosine, Glycine, Aspartic acid, Glutamic acid, Serine, Histidine,
 FT SIGNAL 1 22
 FT CHAIN 23 202
 FT DISULFID 34 156
 FT DISULFID 40 153
 FT DISULFID 82 185
 FT CARBOHYD 31 31
 FT CARBOHYD 56 56
 FT CARBOHYD 85 85
 FT CARBOHYD 95 95
 FT CARBOHYD 118 118
 FT CARBOHYD 138 138
 SQ SEQUENCE 202 AAY 22099 MW 63403 DA 57624 6R3641

Query Match 100.0% Score 25.0 Length 202
 Best Local Similarity 100.0% Pred. No. 33
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 QY 1 DILRG 5
 11111

LB 142 DILRG 146
 RESULT 5
 LB MUSVL
 LB 142 DILRG 146
 AC 662728;
 LB 15-082-1998 (Ref. 37, Created)
 LB 15-082-1998 (Ref. 37, Last sequence update)
 LB 48 MAY 2000 (Ref. 39, Last annotation update)
 LB LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF-
 CN LIF-
 LB Human class (Ameloidosis, etc).
 LB Murkayata; Metastatic chondrosarcoma; Viroblastoma; Ewing's sarcoma;
 LB Hamman-Rich; Bulimia; Carcinoma; Fibrosarcoma; Osteosarcoma;
 LB MCF1_Taxid:9667;
 RN [1]
 RX SEQUENCE FROM N.A.
 RA FISSUR-Endometrium;
 RA MEDLINE:78376158; PubMed:9712113;
 RA Song J.H., Honda A., Murphy R.D.:
 RI "Cloning of leukemia inhibitory factor cDNA and its expression in
 RI the uterus during embryonic diapause and associated leukemia risk
 RI (Mustela vison)."
 RI Mol. Reprod. Dev. 51:113-121(1998).
 CC -1- FUNCTION: LIF HAS THE CAPACITY TO INHIBIT HEMATOPOIETIC DIFFERENTIATION
 CC IN LEUKEMIC CELLS. ITS ACTIVITIES INCLUDE THE INDUCTION OF
 CC HEMATOPOIETIC DIFFERENTIATION IN NORMAL AND MYELOID LEUKEMIA
 CC CELLS, THE INDUCTION OF NEURONAL CELL DIFFERENTIATION, AND THE
 CC STIMULATION OF ACUTE-PHASE PROTEIN SYNTHESIS IN HEPATOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE LIF / OSM FAM IN
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 DR EMBL: M24823; AAC05201.1;
 DR InterPro: IPR001581; LIF_OSM.
 DR Pfam: PF01291; LIF_OSM.1.
 DR SMART: SM00080; LIF_OSM.1.
 DR PROSITE: PS00590; LIF_OSM.1.
 KW Tyrosine, Glycine, Aspartic acid, Glutamic acid, Serine, Histidine,
 FT SIGNAL 1 22
 FT CHAIN 23 202
 FT DISULFID 34 156
 FT DISULFID 40 153
 FT DISULFID 82 185
 FT CARBOHYD 31 31
 FT CARBOHYD 56 56
 FT CARBOHYD 85 85
 FT CARBOHYD 95 95
 FT CARBOHYD 118 118
 SQ SEQUENCE 202 AAY 22114 MW 63403 DA 57624 6R3641

Query Match 100.0% Score 25.0 Length 146
 Best Local Similarity 100.0% Pred. No. 14
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 QY 1 DILRG 5
 11111
 LB 142 DILRG 146
 RESULT 6
 LB EFTU_DILRG
 LB 142 DILRG 146
 AC P50065;
 LB 142 DILRG 146
 AC P50065;

[illegible]

Ref.	Material	Temperature	Time	Atmosphere	Preparation	Characterization
106	EMUL-0004-3	AAAM/PA6				
107	HEB20	PA6/PA66	140°C			
108	100-1	PA6/PA66	180°C/20 h	100% N ₂		
109	PA66	PA6/PA66	210°C/1 h			
110	PA66-11P	PA66-11P	210°C/1 h			
111	PA66-11P	PA66-11P	210°C/1 h			
112	PA66-11P	PA66-11P	210°C/1 h			
113	PA66-11P	PA66-11P	210°C/1 h			
114	PA66-11P	PA66-11P	210°C/1 h			
115	PA66-11P	PA66-11P	210°C/1 h			
116	PA66-11P	PA66-11P	210°C/1 h			
117	PA66-11P	PA66-11P	210°C/1 h			
118	PA66-11P	PA66-11P	210°C/1 h			
119	PA66-11P	PA66-11P	210°C/1 h			
120	PA66-11P	PA66-11P	210°C/1 h			
121	PA66-11P	PA66-11P	210°C/1 h			
122	PA66-11P	PA66-11P	210°C/1 h			
123	PA66-11P	PA66-11P	210°C/1 h			
124	PA66-11P	PA66-11P	210°C/1 h			
125	PA66-11P	PA66-11P	210°C/1 h			
126	PA66-11P	PA66-11P	210°C/1 h			
127	PA66-11P	PA66-11P	210°C/1 h			
128	PA66-11P	PA66-11P	210°C/1 h			
129	PA66-11P	PA66-11P	210°C/1 h			
130	PA66-11P	PA66-11P	210°C/1 h			
131	PA66-11P	PA66-11P	210°C/1 h			
132	PA66-11P	PA66-11P	210°C/1 h			
133	PA66-11P	PA66-11P	210°C/1 h			
134	PA66-11P	PA66-11P	210°C/1 h			
135	PA66-11P	PA66-11P	210°C/1 h			
136	PA66-11P	PA66-11P	210°C/1 h			
137	PA66-11P	PA66-11P	210°C/1 h			
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139	PA66-11P	PA66-11P	210°C/1 h			
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142	PA66-11P	PA66-11P	210°C/1 h			
143	PA66-11P	PA66-11P	210°C/1 h			
144	PA66-11P	PA66-11P	210°C/1 h			
145	PA66-11P	PA66-11P	210°C/1 h			
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148	PA66-11P	PA66-11P	210°C/1 h			
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156	PA66-11P	PA66-11P	210°C/1 h			
157	PA66-11P	PA66-11P	210°C/1 h			
158	PA66-11P	PA66-11P	210°C/1 h			
159	PA66-11P	PA66-11P	210°C/1 h			
160	PA66-11P	PA66-11P	210°C/1 h			
161	PA66-11P	PA66-11P	210°C/1 h			
162	PA66-11P	PA66-11P	210°C/1 h			
163	PA66-11P	PA66-11P				

Property	Method	Time	Space	Input	Output
Correctness	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Completeness	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Soundness	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Consistency	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Reliability	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Stability	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Robustness	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Flexibility	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Adaptability	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Scalability	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Portability	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Interoperability	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Compatibility	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Integration	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Collaboration	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Coordination	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Communication	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Interaction	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Engagement	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Participation	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Involvement	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Contribution	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Impact	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Influence	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Power	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Authority	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Control	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Direction	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Guidance	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Leadership	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Management	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Administration	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Organization	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Structure	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
System	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Framework	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Model	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Template	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Pattern	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Design	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Architecture	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Infrastructure	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Platform	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Environment	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Context	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Situation	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Circumstance	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Condition	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
State	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Form	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Shape	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Structure	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Organization	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
System	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Framework	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Model	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Template	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Pattern	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Design	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Architecture	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Infrastructure	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Platform	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Environment	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Context	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Situation	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Circumstance	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
Condition	Simulation	$O(n^2)$	$O(n)$	Yes	Yes
State	Simulation	$O(n^2)$	$O(n)$	Yes	

[illegible]

PI	COLL	YEAR	STANDARD	PRICE	QTY	AMT
10	100	2000	40	100	4000	4000
11	200	2001	40	100	4000	4000
12	300	2001	40	100	4000	4000
13	400	2001	40	100	4000	4000
14	500	2001	40	100	4000	4000
15	600	2001	40	100	4000	4000
16	700	2001	40	100	4000	4000
17	800	2001	40	100	4000	4000
18	900	2001	40	100	4000	4000
19	1000	2001	40	100	4000	4000
20	1100	2001	40	100	4000	4000
21	1200	2001	40	100	4000	4000
22	1300	2001	40	100	4000	4000
23	1400	2001	40	100	4000	4000
24	1500	2001	40	100	4000	4000
25	1600	2001	40	100	4000	4000
26	1700	2001	40	100	4000	4000
27	1800	2001	40	100	4000	4000
28	1900	2001	40	100	4000	4000
29	2000	2001	40	100	4000	4000
30	2100	2001	40	100	4000	4000
31	2200	2001	40	100	4000	4000
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33	2400	2001	40	100	4000	4000
34	2500	2001	40	100	4000	4000
35	2600	2001	40	100	4000	4000
36	2700	2001	40	100	4000	4000
37	2800	2001	40	100	4000	4000
38	2900	2001	40	100	4000	4000
39	3000	2001	40	100	4000	4000
40	3100	2001	40	100	4000	4000
41	3200	2001	40	100	4000	4000
42	3300	2001	40	100	4000	4000
43	3400	2001	40	100	4000	4000
44	3500	2001	40	100	4000	4000
45	3600	2001	40	100	4000	4000
46	3700	2001	40	100	4000	4000
47	3800	2001	40	100	4000	4000
48	3900	2001	40	100	4000	4000
49	4000	2001	40	100	4000	4000
50	4100	2001	40	100	4000	4000
51	4200	2001	40	100	4000	4000
52	4300	2001	40	100	4000	4000
53	4400	2001	40	100	4000	4000
54	4500	2001	40	100	4000	4000
55	4600	2001	40	100	4000	4000
56	4700	2001	40	100	4000	4000
57	4800	2001	40	100	4000	4000
58	4900	2001	40	100	4000	4000
59	5000	2001	40	100	4000	4000
60	5100	2001	40	100	4000	4000
61	5200	2001	40	100	4000	4000
62	5300	2001	40	100	4000	4000
63	5400	2001	40	100	4000	4000
64	5500	2001	40	100	4000	4000
65	5600	2001	40	100	4000	4000

[1] $\mathcal{H}_p(\mathbb{R}^n)$ defined by the norm $\|f\|_p = \left(\int_{\mathbb{R}^n} |f(x)|^p dx \right)^{1/p}$, $1 \leq p < \infty$, and ∞ -norm $\|f\|_\infty = \text{ess sup}_{x \in \mathbb{R}^n} |f(x)|$.
[2] Sobolev (1938) (1975) The $M^{p,2}$ -norms/| Δ | s are defined as

[illegible]

These two methods are complementary to each other, and together they provide a more complete picture of the microclimate and the physical characteristics of the forest in the study area. Both methods have their own strengths and weaknesses. The microclimate method is more precise and can provide detailed information about the microclimate, but it is more labor-intensive and requires specialized equipment. The physical characteristics method is less precise but is easier to implement and can provide a broader overview of the forest structure. By combining these two methods, we can obtain a more comprehensive understanding of the forest environment.

Keywords: child sexual abuse; disclosure; self-blame; social support

Year	Math	Science	Reading	Writing	History	Art	Music	Physical Education	Foreign Languages	Health	Life Science	Environmental Science	Technology	Other
1990	100	95	90	85	80	75	70	65	60	55	50	45	40	35
1995	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2000	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2005	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2010	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2015	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2020	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2025	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2030	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2035	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2040	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2045	100	95	90	85	80	75	70	65	60	55	50	45	40	35
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2055	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2060	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2065	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2070	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2075	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2080	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2085	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2090	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2095	100	95	90	85	80	75	70	65	60	55	50	45	40	35
2100	100	95	90	85	80	75	70	65	60	55	50	45	40	35

2007		2008		2009		2010		2011		2012		2013		2014		2015		2016		2017		2018		2019		2020		2021		2022		2023		2024		2025		2026		2027		2028		2029		2030		2031		2032		2033		2034		2035		2036		2037		2038		2039		2040		2041		2042		2043		2044		2045		2046		2047		2048		2049		2050		2051		2052		2053		2054		2055		2056		2057		2058		2059		2060		2061		2062		2063		2064		2065		2066		2067		2068		2069		2070		2071		2072		2073		2074		2075		2076		2077		2078		2079		2080		2081		2082		2083		2084		2085		2086		2087		2088		2089		2090		2091		2092		2093		2094		2095		2096		2097		2098		2099		2100	
2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																														

[illegible][illegible]

the following cases: (a) $\beta = 0$, (b) $\beta = 1$, (c) $\beta = 2$, (d) $\beta = 3$, (e) $\beta = 4$, (f) $\beta = 5$, (g) $\beta = 6$, (h) $\beta = 7$, (i) $\beta = 8$, (j) $\beta = 9$, (k) $\beta = 10$, (l) $\beta = 11$, (m) $\beta = 12$, (n) $\beta = 13$, (o) $\beta = 14$, (p) $\beta = 15$, (q) $\beta = 16$, (r) $\beta = 17$, (s) $\beta = 18$, (t) $\beta = 19$, (u) $\beta = 20$, (v) $\beta = 21$, (w) $\beta = 22$, (x) $\beta = 23$, (y) $\beta = 24$, (z) $\beta = 25$, (aa) $\beta = 26$, (ab) $\beta = 27$, (ac) $\beta = 28$, (ad) $\beta = 29$, (ae) $\beta = 30$, (af) $\beta = 31$, (ag) $\beta = 32$, (ah) $\beta = 33$, (ai) $\beta = 34$, (aj) $\beta = 35$, (ak) $\beta = 36$, (al) $\beta = 37$, (am) $\beta = 38$, (an) $\beta = 39$, (ao) $\beta = 40$, (ap) $\beta = 41$, (aq) $\beta = 42$, (ar) $\beta = 43$, (as) $\beta = 44$, (at) $\beta = 45$, (au) $\beta = 46$, (av) $\beta = 47$, (aw) $\beta = 48$, (ax) $\beta = 49$, (ay) $\beta = 50$, (az) $\beta = 51$, (ba) $\beta = 52$, (bb) $\beta = 53$, (bc) $\beta = 54$, (bd) $\beta = 55$, (be) $\beta = 56$, (bf) $\beta = 57$, (bg) $\beta = 58$, (bh) $\beta = 59$, (bi) $\beta = 60$, (bj) $\beta = 61$, (bk) $\beta = 62$, (bl) $\beta = 63$, (bm) $\beta = 64$, (bn) $\beta = 65$, (bo) $\beta = 66$, (bp) $\beta = 67$, (bq) $\beta = 68$, (br) $\beta = 69$, (bs) $\beta = 70$, (bt) $\beta = 71$, (bu) $\beta = 72$, (bv) $\beta = 73$, (bw) $\beta = 74$, (bx) $\beta = 75$, (by) $\beta = 76$, (bz) $\beta = 77$, (ca) $\beta = 78$, (cb) $\beta = 79$, (cc) $\beta = 80$, (cd) $\beta = 81$, (ce) $\beta = 82$, (cf) $\beta = 83$, (cg) $\beta = 84$, (ch) $\beta = 85$, (ci) $\beta = 86$, (cj) $\beta = 87$, (ck) $\beta = 88$, (cl) $\beta = 89$, (cm) $\beta = 90$, (cn) $\beta = 91$, (co) $\beta = 92$, (cp) $\beta = 93$, (cq) $\beta = 94$, (cr) $\beta = 95$, (cs) $\beta = 96$, (ct) $\beta = 97$, (cu) $\beta = 98$, (cv) $\beta = 99$, (cw) $\beta = 100$, (cx) $\beta = 101$, (cy) $\beta = 102$, (cz) $\beta = 103$, (da) $\beta = 104$, (db) $\beta 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1996	USA	0.0000	0.0000
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2007	USA	0.0000	0.0000
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2011	USA	0.0000	0.0000
2012	USA	0.0000	0.0000
2013	USA	0.0000	0.0000
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2016	USA	0.0000	0.0000
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QY 1 DILLIG 5
DB 123 DILLIG 127

RESULT 9
YC47_HELPJ
ID YC47_HELPJ STANDARD: PRI: 440 AA
AC 092400:
DT 30-MAY-2000 (rel: 39, checked)
DI 40-MAY-2000 (rel: 39, last sequence update)
DT 20-AUG-2001 (rel: 40, last annotation update)
DE PROTEIN HP1156.
GN HP1156.
OS Helicobacter pylori J99 (Campylobacter J99 str. J99)
OC Bacteria; Proteobacteria; epsilon subdivision; helicobacter group;
OC Helicobacter;
OX NCBI_TaxID=859643.
RP SEQUENCE FROM N.A.
RX MEDLINE:99120557; PubMed 9924822.
RA Alm R.A., Ling L.S.L., Moll D.T., King B.L., Brown E.B., Doid P.C.,
RA Smith D.R., Norman B., Gold H.C., deGange B., Daniel G.,
RA Tumme P.J., Casuso A., Ulla-Nickelsen M., Fries D.M., Ivers P.,
KA Gibson K., Metherell D., Mills S.D., Jiang J., Jolly D.E., Vovis G.F.,
KA Trust J.O.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen helicobacter pylori."
RL Nature 357:176-180(1999)
RN [2]
RP INTERACTION.
KA Location P.1.
RL Unpublished observations (Apr-2000).
CC 1- FUNCTION: COULD BE THE FUNCTIONAL EQUIVANT OF ENA POLYPEPTASE 111
CC DELTA SUBUNIT (HNA).
CC 1- SUBUNIT: SEEMS TO INTERACT WITH H. PYLORI HNA.
CC*
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CC or send an email to license@ebi.ac.uk).
CC
DR EMBL: A0001541; AAD06742.1.
KW Transferring RNA directed RNA polymerase; Ena; Polypeptase;
KW Complete proteome.
SO SPOUNCE 340 AA; 3954 + MW: 68639012722016 GP064;

Query Match 100.0% Score 250 DB: Length 440
Best Local Similarity 100.0% Pred. No. 672
Matches 52 Conservative 02 Mismatches 0 Indels 04 Gaps 02

QY 1 DILLIG 5
DB 250 DILLIG 254

RESULT 10
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ID YC47_HELPJ STANDARD: PRI: 440 AA
AC 092400:
DT 30-MAY-2000 (rel: 39, checked)
DI 40-MAY-2000 (rel: 39, last sequence update)
DT 20-AUG-2001 (rel: 40, last annotation update)
DE PROTEIN HP1247.
GN HP1247.
OS Helicobacter pylori (Campylobacter pylori)
OC Bacteria; Proteobacteria; epsilon subdivision; helicobacter group;
OC Helicobacter;
OX NCBI_TaxID=859643.

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OX NCBI_TaxID 2 859643
GN 111
RP SEQUENCE FROM N.A.
RX STRAIN 26675 / ARO1 700422;
RX MEDLINE:97394467; PubMed 9752185;
KA Lomb J.-P., White G., Kottmann A.B., O'Garra A., Scott M.,
KA Probstman E.D., Kottmann A.B., O'Garra A., Scott M.,
KA Nelson K., Kottmann A.B., O'Garra A., Scott M.,
KA Lottus B., Richardson B., Jackson R., Kottmann A.B.,
KA McKenney K., Richardson B., Jackson R., Kottmann A.B.,
KA Berg D.E., O'Garra A.B., O'Garra A.B., O'Garra A.B.,
KA O'Garra A.B., O'Garra A.B., O'Garra A.B., O'Garra A.B.,
KA Hayes W.S., O'Garra A.B., O'Garra A.B., O'Garra A.B.,
KA Verter J.C.;
RT "The complete genome sequence of the gastric pathogen bacterium
RT pylori."
RL Nature 386:539-547(1997).
RN [2]
RP INTERACTION.
KA Location P.1.
RL Unpublished observations (Apr-2000).
CC 1- FUNCTION: COULD BE THE FUNCTIONAL EQUIVANT OF ENA POLYPEPTASE 111
CC DELTA SUBUNIT (HNA).
CC 1- SUBUNIT: SEEMS TO INTERACT WITH H. PYLORI HNA.
CC*
CC This SWISS-Prot entry is copyright. It is provided through a collaboration
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CC entities requires a license agreement (see http://www.ebi.ac.uk
CC or send an email to license@ebi.ac.uk).
CC
DR EMBL: A000640; AAD06742.1.
KW Transferring RNA directed RNA polymerase; Ena; Polypeptase;
KW Complete proteome.
SO SPOUNCE 440 AA; 3954 + MW: 68639012722016 GP064;

Query Match 100.0% Score 250 DB: Length 440
Best Local Similarity 100.0% Pred. No. 672
Matches 52 Conservative 02 Mismatches 0 Indels 04 Gaps 02

QY 1 DILLIG 5
DB 250 DILLIG 254

RESULT 11
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ID AR0A_STIRN STANDARD: PRI: 440 AA
AC 092400:
DT 30-MAY-2000 (rel: 39, checked)
DI 40-MAY-2000 (rel: 39, last sequence update)
DT 20-AUG-2001 (rel: 40, last annotation update)
DE PROTEIN HP1247.
GN HP1247.
OS Helicobacter pylori (Campylobacter pylori)
OC Bacteria; Proteobacteria; epsilon subdivision; helicobacter group;
OC Helicobacter;
OX NCBI_TaxID 111
RP SEQUENCE FROM N.A.
RX Alm R.A., Ling L.S.L., Moll D.T., King B.L., Brown E.B., Doid P.C.,
KA Kallender H., Payne I.J.;
RT "Characterization of streptococcus pneumoniae serotype 9V by a
RT 3 phosphate synthase and its activation by a mutant of
RT submitted (Jul-1999) to the EMBL/GenBank/ENA database.
CC 1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + H2O = 3-phospho-D-glucose
CC 1- ORIGIN: SWITZERLAND (1) (1) MARXWERT
CC 1- PATHWAY: SIXTH STEP IN THE GLYCOLYSIS OF GLUCOSE WITHIN

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DR SMART: SMO0248; ANK: 6;
 DR PROSITE: PS00088; ANK_REPEAT: 5;
 DR PROSITE: PS0297; ANK_REPEAT: 1;
 KW PROTOGENOMES: Chromosomal transcription factor; ANK repeat;
 KW Nucleic protein; transcription regulation; ANK repeat; Phosphorylation;
 FI DOMAIN: 1-112; PRO-RICH;
 FI REPEAT: 124-155; ANK 1;
 FI REPEAT: 163-192; ANK 2;
 FI REPEAT: 196-227; ANK 3;
 FI REPEAT: 232-262; ANK 4;
 FI REPEAT: 267-296; ANK 5;
 FI REPEAT: 300-329; ANK 6;
 FI DOMAIN: 357-446; SH2/TK-REC;
 SI SPECIFIC: 445 AA; 16799 MW; 61AA/27171AA/16799 MW;
 Query Match: 100.0%; Score: 25; Eph: 1; Length: 446;
 Best Local Similarity: 100.0%; Prot. No.: 752;
 Matches: 5; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;
 QY 1 DILRG 5
 1111
 DB 348 DILRG 352
 RESULT 14
 DNL_THEME STANDARD: PRI: 688 AA.
 AC QWXXV;
 DT 30-MAY-2000 (Ref: 39, *Updated)
 DT 30-MAY-2000 (Ref: 39, Last sequence update)
 DT 20-AUG-2001 (Ref: 40, Last annotation update)
 DE DNA J1456 (EC 5.5.1.2) (GARYDAKIS AND LESTER) STANDARD (NA-1);
 GN DNA or TM0100;
 OS Thermotoga maritima;
 NC Bacteria; Thermotogales; Thermotoga;
 CX NCBI_TaxID=2336;
 KN 111
 KP SOURCE: FROM N.A.
 RP STRAIN: MSB / DSM 3109;
 RA MEDLINE: 99287316; PubMed: 1060571;
 RA NELSON K.E., CLAYTON K.A., GILL S.R., GILMAN M., BODMAN R.,
 RA HILL D., HICKEY E.K., PETERSON J.P., NELSON K.E., KETCHUM K.A.,
 RA McBRIDE L., UTTERBACK W., WATKINS J.A., LINGG K.D., GORDON M.M.,
 RA Stewart A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
 RA Heideberg J., Sutton G.G., Fleischmann R.D., Nelson J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser J.M.;
 FT "Evidence for lateral gene transfer between Archaea and Bacteria from
 FT genome sequence of Thermotoga maritima.";
 RL Nature 399:323-329 (1999).
 CC -1- FUNCTION: THIS PROTEIN CATALYZES THE PHOSPHORYLATION OF
 CC LIPIDS BETWEEN THE C-2 AND C-3 OF A Glycerol Phospholipid
 CC STRAIGHT CHAIN USING NAD+ AS A COFACTOR AND A THIOESTER-DEPENDENT
 CC THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND REPAIR OF
 CC DAMAGED DNA (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: NAD(+) - (DEPHOSPHORYLATING) N-
 CC (DEOXYRIBOSYL)ADENINE AMP + NUCLEOTIDE PHOSPHATE
 CC (DEOXYRIBOSYL)ADENINE)
 CC -1- SIMILARITY: BELONGS TO THE NAD-DEPENDENT DNA-ATASE FAMILY.
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 CC or send an email to license@ebi.ac.uk.
 CC EMBL: AF001666; A005194.1;
 DR TIGR: TM0100;
 DR InterPro: IPR001357; BRCT;
 DR InterPro: IPR001679; DNA_Ligase_N;
 DR InterPro: IPR000445; HHH.

DR InterPro: IPR000445; HHH;
 DR InterPro: IPR005343; BRCT;
 DR InterPro: IPR014573; DNA_Ligase_N;
 DR InterPro: IPR005343; HHH;
 DR PROSITE: PS003944; DNA_Ligase_N_1;
 DR SMART: SMO0292; BRCT: 1;
 DR SMART: SMO0278; HHH: 2;
 DR SMART: SMO02522; DNA_N_1;
 DR PROSITE: PS01722; BRCT: 1;
 DR PROSITE: PS01953; BRCT_1;
 DR PROSITE: PS01953; BRCT_1;
 KW LIGASE DNA REPAIR; DNA REPLICATION; DNA REPAIR; DNA REPAIR;
 FI BRCT: 120-155; ANK 1;
 SI SPECIFIC: 445 AA; 16799 MW; 61AA/27171AA/16799 MW;
 Query Match: 100.0%; Score: 25; Eph: 1; Length: 446;
 Best Local Similarity: 100.0%; Prot. No.: 752;
 Matches: 5; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;
 QY 1 DILRG 5
 1111
 DB 593 DILRG 592
 RESULT 15
 LKTA_ACTIN STANDARD: PRI: 105 AA.
 AC P16462;
 DT 01-NOV-1990 (Ref: 1, *Updated)
 DT 01-NOV-1990 (Ref: 1, Last sequence update)
 DT 30-MAY-2000 (Ref: 3, Last annotation update)
 DE LKTA or LTA;
 GN Actinobacillus actinoyes; Actinobacillus (Lactobacillus)
 OS Actinobacillus actinoyes; Actinobacillus (Lactobacillus)
 NC Bacteria; Proteobacteria; Gamma; Actinobacillus;
 CX NCBI_TaxID=714;
 KN 111
 KP SOURCE: FROM N.A.
 RP STRAIN: JP2;
 RA MEDLINE: 89359482; PubMed: 2670940;
 RA LALLY E.T., GOLDBERGER, KROBIA L.R., LALLEMAN N.S., ROSENBLUM D.,
 RA ROSENBLUM J.C., CHASE, C.W., BODMAN D.K.;
 RA "Analysis of the Actinobacillus actinoyes genome and the role of
 RA genes, deletion of unique features and the presence of a
 RA toxin.";
 RL J. Biol. Chem. 264:1645-1649 (1989).
 CC -1- FUNCTION: THIS PROTEIN IS A MEMBER OF THE ACTIN
 CC FAMILY. IT IS A MEMBER OF THE ACTIN FAMILY AND IS A MEMBER OF
 CC THE ACTIN FAMILY. IT IS A MEMBER OF THE ACTIN FAMILY AND IS A
 CC MEMBER OF THE ACTIN FAMILY. IT IS A MEMBER OF THE ACTIN FAMILY
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 CC MEMBER OF THE ACTIN FAMILY. IT IS A MEMBER OF THE ACTIN FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
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 CC or send an email to license@ebi.ac.uk.
 CC EMBL: M27399; AA01722.1;

09/01/15 09:00:15 PRELIMINARY: PRI: 141 AA

AT 09:00:15

DT 01-JUN-2001 (FEBM001, 17, created)

DT 01-JUN-2001 (FEBM001, 17, last sequence update)

D1 01-JUN-2001 (FEBM001, 17, last annotation update)

D2 251004806R1K PROTEIN.

D3 251004806R1K

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

OX NCBI_taxid:10090.

RN 11

RP SEQUENCE FROM N.A.

RC STEADY STATE: 100% EMBL: AK142961, EMBL: AK142962, EMBL: AK142963, EMBL: AK142964, EMBL: AK142965, EMBL: AK142966, EMBL: AK142967, EMBL: AK142968, EMBL: AK142969, EMBL: AK142970, EMBL: AK142971, EMBL: AK142972, EMBL: AK142973, EMBL: AK142974, EMBL: AK142975, EMBL: AK142976, EMBL: AK142977, EMBL: AK142978, EMBL: AK142979, EMBL: AK142980, EMBL: AK142981, EMBL: AK142982, EMBL: AK142983, EMBL: AK142984, EMBL: AK142985, EMBL: AK142986, EMBL: AK142987, EMBL: AK142988, EMBL: AK142989, EMBL: AK142990, EMBL: AK142991, EMBL: AK142992, EMBL: AK142993, EMBL: AK142994, EMBL: AK142995, EMBL: AK142996, EMBL: AK142997, EMBL: AK142998, EMBL: AK142999, EMBL: AK143000, EMBL: AK143001, EMBL: AK143002, EMBL: AK143003, EMBL: AK143004, EMBL: AK143005, EMBL: AK143006, EMBL: AK143007, EMBL: AK143008, EMBL: AK143009, EMBL: AK143010, EMBL: AK143011, EMBL: AK143012, EMBL: AK143013, EMBL: AK143014, EMBL: AK143015, EMBL: AK143016, EMBL: AK143017, EMBL: AK143018, EMBL: AK143019, EMBL: AK143020, EMBL: AK143021, 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7A. [REDACTED] [REDACTED]
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8A. [REDACTED] [REDACTED]
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